

SEQUENCE SEARCH SUMMARY 10/790224

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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:03:48 ; Search time 173 Seconds
(without alignments)
1066.386 Million cell updates/sec

Title: US-10-790-224A-20
Perfect score: 2517
Sequence: 1 VAFETPEEIVKFIKDENEVEF.....EISPVRLRPTPQEFELYFDC 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2517	100.0	477	8	ADP87712 Adp87712 Brevibact
2	2517	100.0	477	8	ADS73714 Ads73714 B. lactof
3	2516	100.0	477	4	AAB79682 Aab79682 Corynebact
4	2513	99.8	477	4	AAG93231 Aag93231 C glutami
5	2036.5	80.9	478	6	ABU25851 Abu25851 Protein e
6	1790.5	71.1	478	2	AAW63035 Aaw63035 Mycobacte
7	1790.5	71.1	478	2	AAW37901 Aaw37901 Mycobacte
8	1789.5	71.1	478	7	ADF18438 Adf18438 Mycobacte
9	1784.5	70.9	478	2	AAW18160 Aaw18160 Mycobacte

EP1106790
6985 dm29

10	1784.5	70.9	478	7	AAE39352	Aae39352	M. tuberc
11	1618	64.3	478	5	ABP65893	Abp65893	Bifidobac
12	1555.5	61.8	533	4	AAU54574	Aau54574	Propionib
13	1555.5	61.8	533	6	ABM51093	Abm51093	Propionib
14	1253.5	49.8	469	6	ABU49639	Abu49639	Protein e
15	1236.5	49.1	471	6	ABU19549	Abu19549	Protein e
16	1235.5	49.1	499	6	ABU23390	Abu23390	Protein e
17	1234.5	49.0	469	6	ABU33405	Abu33405	Protein e
18	1232.5	49.0	469	6	ABU28077	Abu28077	Protein e
19	1230.5	48.9	470	6	ABM70321	Abm70321	Photorhab
20	1227.5	48.8	469	6	ABU50092	Abu50092	Protein e
21	1226.5	48.7	471	6	ABU22059	Abu22059	Protein e
22	1223.5	48.6	469	6	ABU31549	Abu31549	Protein e
23	1221.5	48.5	476	7	ABO65700	Abo65700	Klebsiell
24	1216.5	48.3	469	4	AAU38196	Aau38196	Salmonell
25	1216.5	48.3	469	6	ABU48136	Abu48136	Protein e
26	1215.5	48.3	468	7	ADI53075	Adi53075	E. coli g
27	1215.5	48.3	469	4	AAU34825	Aau34825	E. coli c
28	1215.5	48.3	469	6	ABU28844	Abu28844	Protein e
29	1215.5	48.3	469	8	ADI38944	Adi38944	Glutamine
30	1214.5	48.3	469	6	ABU45561	Abu45561	Protein e
31	1201.5	47.7	469	6	ABU40915	Abu40915	Protein e
32	1201.5	47.7	493	7	ADF06469	Adf06469	Bacterial
33	1188	47.2	468	6	ABU40023	Abu40023	Protein e
34	1181	46.9	511	6	ABU37246	Abu37246	Protein e
35	1181	46.9	524	6	ABP80864	Abp80864	N. gonorr
36	1176	46.7	468	6	ABU41641	Abu41641	Protein e
37	1176	46.7	472	6	ABU38151	Abu38151	Protein e
38	1173	46.6	472	8	ADP08211	Adp08211	Neisseria
39	1165	46.3	469	4	AAU36495	Aau36495	Pseudomon
40	1165	46.3	469	6	ABU38863	Abu38863	Protein e
41	1163	46.2	471	6	ABU16678	Abu16678	Protein e
42	1163	46.2	489	6	ADA33076	Ada33076	Acinetoba
43	1159.5	46.1	472	4	AAU35544	Aau35544	Haemophil
44	1159.5	46.1	472	6	ABU30408	Abu30408	Protein e
45	1159.5	46.1	472	6	ABU39284	Abu39284	Protein e

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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:13:35 ; Search time 43 Seconds
(without alignments)
828.084 Million cell updates/sec

Title: US-10-790-224A-20
Perfect score: 2517
Sequence: 1 VAFETPEEIVKFIKDENVF.....EISPVRLRPTQEFELYFDC 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1221.5	48.5	476	4	US-09-489-039A-12217	Sequence 12217, A
2	1201.5	47.7	493	4	US-09-543-681A-6754	Sequence 6754, Ap
3	1163	46.2	489	4	US-09-328-352-4363	Sequence 4363, Ap
4	1153.5	45.8	481	4	US-09-252-991A-32811	Sequence 32811, A
5	1122	44.6	476	4	US-09-540-236-2406	Sequence 2406, Ap
6	722.5	28.7	448	4	US-09-583-110-4662	Sequence 4662, Ap
7	722	28.7	446	4	US-09-710-279-2250	Sequence 2250, Ap
8	722	28.7	452	3	US-09-134-001C-4173	Sequence 4173, Ap
9	499	19.8	241	4	US-09-134-000C-4967	Sequence 4967, Ap
10	457	18.2	531	4	US-09-252-991A-26690	Sequence 26690, A
11	430	17.1	275	4	US-09-107-532A-6200	Sequence 6200, Ap

12	429.5	17.1	479	4	US-09-902-540-15979	Sequence 15979, A
13	407.5	16.2	464	4	US-09-252-991A-27559	Sequence 27559, A
14	405.5	16.1	250	4	US-09-107-433-4225	Sequence 4225, Ap
15	401.5	16.0	489	4	US-09-252-991A-27833	Sequence 27833, A
16	388	15.4	464	4	US-09-252-991A-28048	Sequence 28048, A
17	348	13.8	190	4	US-09-107-532A-4613	Sequence 4613, Ap
18	341	13.5	449	4	US-09-252-991A-17901	Sequence 17901, A
19	338.5	13.4	491	4	US-09-252-991A-19014	Sequence 19014, A
20	313.5	12.5	661	4	US-09-252-991A-18960	Sequence 18960, A
21	275.5	10.9	480	4	US-09-328-352-6949	Sequence 6949, Ap
22	268.5	10.7	520	4	US-09-949-016-7107	Sequence 7107, Ap
23	249.5	9.9	1037	4	US-09-252-991A-16796	Sequence 16796, A
24	242	9.6	208	4	US-09-902-540-9748	Sequence 9748, Ap
25	222.5	8.8	257	4	US-09-489-039A-7508	Sequence 7508, Ap
26	157.5	6.3	97	4	US-09-107-433-4285	Sequence 4285, Ap
27	156	6.2	401	4	US-09-949-016-7956	Sequence 7956, Ap
28	139.5	5.5	356	4	US-09-786-534-2	Sequence 2, Appli
29	132	5.2	383	4	US-09-248-796A-17492	Sequence 17492, A
30	129	5.1	387	4	US-09-270-767-42090	Sequence 42090, A
31	104.5	4.2	796	4	US-09-107-532A-7065	Sequence 7065, Ap
32	104	4.1	139	4	US-09-107-433-4038	Sequence 4038, Ap
33	101.5	4.0	599	4	US-09-543-681A-4524	Sequence 4524, Ap
34	100	4.0	232	4	US-09-489-039A-7457	Sequence 7457, Ap
35	99.5	4.0	760	3	US-09-323-872A-31	Sequence 31, Appl
36	99.5	4.0	760	4	US-09-072-433-35	Sequence 35, Appl
37	99	3.9	3290	4	US-09-328-352-5486	Sequence 5486, Ap
38	98.5	3.9	765	4	US-09-489-039A-12098	Sequence 12098, A
39	98	3.9	452	1	US-08-434-702-6	Sequence 6, Appli
40	98	3.9	452	1	US-08-271-883-6	Sequence 6, Appli
41	96	3.8	1548	4	US-09-252-991A-22301	Sequence 22301, A
42	95	3.8	3724	2	US-08-804-227C-10	Sequence 10, Appl
43	95	3.8	3724	2	US-08-804-198-4	Sequence 4, Appli
44	94	3.7	448	4	US-09-878-766A-22	Sequence 22, Appl
45	93	3.7	854	4	US-09-949-016-11363	Sequence 11363, A

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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:19:50 ; Search time 143 Seconds
(without alignments)
1106.082 Million cell updates/sec

Title: US-10-790-224A-20
Perfect score: 2517
Sequence: 1 VAFETPEEIVKFIKDENEVEF.....EISPVRLRPTPQEFELYFDC 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 8
Query

No.	Score	Match	Length	DB	ID	Description
1	2517	100.0	477	16	US-10-720-177-4	Sequence 4, Appli
2	2517	100.0	477	17	US-10-790-224A-20	Sequence 20, Appl
3	2513	99.8	477	9	US-09-738-626-6985	Sequence 6985, Ap
4	2036.5	80.9	478	15	US-10-282-122A-53775	Sequence 53775, A
5	1642.5	65.3	469	14	US-10-156-761-13532	Sequence 13532, A
6	1253.5	49.8	469	15	US-10-282-122A-77563	Sequence 77563, A
7	1236.5	49.1	471	15	US-10-282-122A-47473	Sequence 47473, A
8	1235.5	49.1	499	15	US-10-282-122A-51314	Sequence 51314, A
9	1234.5	49.0	469	15	US-10-282-122A-61329	Sequence 61329, A
10	1232.5	49.0	469	15	US-10-282-122A-56001	Sequence 56001, A
11	1227.5	48.8	469	15	US-10-282-122A-78016	Sequence 78016, A
12	1226.5	48.7	471	15	US-10-282-122A-49983	Sequence 49983, A
13	1223.5	48.6	469	15	US-10-282-122A-59473	Sequence 59473, A
14	1216.5	48.3	469	9	US-09-815-242-13789	Sequence 13789, A
15	1216.5	48.3	469	15	US-10-282-122A-76060	Sequence 76060, A
16	1215.5	48.3	468	14	US-10-299-799-1	Sequence 1, Appli
17	1215.5	48.3	469	9	US-09-815-242-10418	Sequence 10418, A
18	1215.5	48.3	469	15	US-10-282-122A-56768	Sequence 56768, A
19	1215.5	48.3	469	15	US-10-612-779-89	Sequence 89, Appl
20	1214.5	48.3	469	15	US-10-282-122A-73485	Sequence 73485, A
21	1201.5	47.7	469	15	US-10-282-122A-68839	Sequence 68839, A
22	1188	47.2	468	15	US-10-282-122A-67947	Sequence 67947, A
23	1181	46.9	511	15	US-10-282-122A-65170	Sequence 65170, A
24	1176	46.7	468	15	US-10-282-122A-69565	Sequence 69565, A
25	1176	46.7	472	15	US-10-282-122A-66075	Sequence 66075, A
26	1165	46.3	469	9	US-09-815-242-12088	Sequence 12088, A
27	1165	46.3	469	15	US-10-282-122A-66787	Sequence 66787, A
28	1163	46.2	471	15	US-10-282-122A-44602	Sequence 44602, A
29	1159.5	46.1	472	9	US-09-815-242-11137	Sequence 11137, A
30	1159.5	46.1	472	15	US-10-282-122A-58332	Sequence 58332, A
31	1159.5	46.1	472	15	US-10-282-122A-67208	Sequence 67208, A
32	1139.5	45.3	448	15	US-10-282-122A-49184	Sequence 49184, A
33	1122	44.6	469	15	US-10-282-122A-63077	Sequence 63077, A
34	1086.5	43.2	476	15	US-10-282-122A-54398	Sequence 54398, A
35	1048	41.6	481	9	US-09-815-242-11507	Sequence 11507, A
36	1048	41.6	481	15	US-10-282-122A-58725	Sequence 58725, A
37	1048	41.6	481	15	US-10-335-977-6523	Sequence 6523, Ap
38	811	32.2	446	15	US-10-282-122A-58019	Sequence 58019, A
39	803.5	31.9	444	15	US-10-282-122A-45823	Sequence 45823, A
40	787	31.3	446	15	US-10-282-122A-57203	Sequence 57203, A
41	787	31.3	451	9	US-09-815-242-10514	Sequence 10514, A
42	782.5	31.1	444	15	US-10-282-122A-45990	Sequence 45990, A
43	765	30.4	439	15	US-10-369-493-2983	Sequence 2983, Ap
44	762.5	30.3	448	15	US-10-282-122A-72256	Sequence 72256, A
45	753	29.9	444	15	US-10-282-122A-60735	Sequence 60735, A

09/788625
6985

ALIGNMENTS

RESULT 1

US-10-720-177-4

; Sequence 4, Application US/10720177

; Publication No. US20040152175A1

; GENERAL INFORMATION:

; APPLICANT: NAKAMURA, Jun

; APPLICANT: AKIYAMA, Kayo

; TITLE OF INVENTION: Method for Producing L-Glutamine and L-Glutamine
Producing Bacteria

; FILE REFERENCE: OP1637-US

; CURRENT APPLICATION NUMBER: US/10/720,177

; CURRENT FILING DATE: 2003-11-25

; PRIOR APPLICATION NUMBER: JP 2002-342287

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 477

; TYPE: PRT

; ORGANISM: Brevibacterium flavum

US-10-720-177-4

Query Match 100.0%; Score 2517; DB 16; Length 477;

Best Local Similarity 100.0%; Pred. No. 1.5e-228;

Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 VAFETPEEIVKFIKDENVFVDVRFTDLPGTEQHFSIPAASFDADTVEEGLAFDGSSIRG 60

Qy     61 FTTIDESDMNLLPDLGTATLDPFRKAKTLNVKFFVHDPFTREAFSRDPRNVARKAEQYLA 120
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Db     61 FTTIDESDMNLLPDLGTATLDPFRKAKTLNVKFFVHDPFTREAFSRDPRNVARKAEQYLA 120

Qy    121 STGIADTCNFGAEAEFYLFDSVRYSTEMNSGFYEVDTEEGWWNRGKETNLDGTPNLGAKN 180
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Db    121 STGIADTCNFGAEAEFYLFDSVRYSTEMNSGFYEVDTEEGWWNRGKETNLDGTPNLGAKN 180

Qy    181 RVKGGYFPVAPYDQTVDVRDDMVRNLAASGFALERFHHEVGGGQQEINYRFNTMLHAADD 240
      |||
Db    181 RVKGGYFPVAPYDQTVDVRDDMVRNLAASGFALERFHHEVGGGQQEINYRFNTMLHAADD 240

Qy    241 IQTFKYIIKN TARLHGKAATFMPKPLAGDNGSGMHAHQSLWKDGKPLFHDESGYAGLSDI 300
      |||
Db    241 IQTFKYIIKN TARLHGKAATFMPKPLAGDNGSGMHAHQSLWKDGKPLFHDESGYAGLSDI 300

Qy    301 ARYYIGGILHHAGAVLAFTNATLNSYHRLVPGFEAPINLVYSQRNRSAAVRIPITGSNPK 360
      |||
Db    301 ARYYIGGILHHAGAVLAFTNATLNSYHRLVPGFEAPINLVYSQRNRSAAVRIPITGSNPK 360

Qy    361 AKRIEFRAPDPSGNPYLGFAAMMMAGLDGIKNRIEPHAPVDKDLIELPPEEAASIPQAPT 420
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Db    361 AKRIEFRAPDPSGNPYLGFAAMMMAGLDGIKNRIEPHAPVDKDLIELPPEEAASIPQAPT 420
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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:04:39 ; Search time 45 Seconds
(without alignments)
1019.898 Million cell updates/sec

Title: US-10-790-224A-20
Perfect score: 2517
Sequence: 1 VAFETPEEIVKFIKDENVF.....EISPVRLRPTPQEFELYFDC 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	1789.5	71.1	478	2	H70775	probable glutamine
2	1654.5	65.7	469	1	AJSMQC	glutamate-ammonia
3	1592.5	63.3	469	2	S32024	glutamate-ammonia
4	1516	60.2	474	2	A40598	glutamate-ammonia
5	1412.5	56.1	473	2	S75141	glutamate-ammonia
6	1394	55.4	471	2	JC1403	glutamate-ammonia
7	1380.5	54.8	473	2	A47050	glutamate-ammonia
8	1363.5	54.2	474	1	AJAIQ	glutamate-ammonia
9	1363.5	54.2	474	2	AI2096	glutamate-ammonia
10	1266	50.3	469	2	G70310	glutamate-ammonia
11	1253.5	49.8	469	2	A82038	glutamate-ammonia
12	1252	49.7	468	1	AJVCQA	glutamate-ammonia
13	1227.5	48.8	469	2	AI0003	glutamate-ammonia

14	1223.5	48.6	469	1	AJEBQT	glutamate-ammonia
15	1216.5	48.3	469	2	AI0949	glutamine syntheta
16	1215.5	48.3	469	1	AJECQ	glutamate-ammonia
17	1215.5	48.3	469	2	H91227	glutamine syntheta
18	1211.5	48.1	469	2	G86074	glutamine syntheta
19	1211	48.1	469	2	AC2794	glutamine syntheta
20	1211	48.1	469	2	B97573	glutamine syntheta
21	1204.5	47.9	469	2	S23899	glutamate-ammonia
22	1197.5	47.6	468	1	AJKCQB	glutamate-ammonia
23	1184	47.0	468	2	A37176	glutamate-ammonia
24	1182.5	47.0	467	1	AJAVQ	glutamate-ammonia
25	1176	46.7	472	2	E81784	glutamate-ammonia
26	1173	46.6	472	2	F81208	glutamate-ammonia
27	1171.5	46.5	504	2	G82631	glutamine syntheta
28	1166	46.3	468	1	AJBCQF	glutamate-ammonia
29	1165	46.3	469	2	G83005	glutamine syntheta
30	1162	46.2	469	2	AE3374	glutamate-ammonia
31	1159.5	46.1	472	2	I64098	glutamate-ammonia
32	1159	46.0	469	2	D87493	glutamine syntheta
33	1148	45.6	467	2	S33181	glutamate-ammonia
34	1132	45.0	469	1	AJZRQL	glutamate-ammonia
35	1086.5	43.2	476	2	F81340	glutamate-ammonia
36	1048	41.6	481	2	B71929	glutamine syntheta
37	1048	41.6	481	2	H64583	glutamine syntheta
38	957.5	38.0	471	2	A99180	hypothetical prote
39	956.5	38.0	471	2	S11899	glutamate-ammonia
40	806.5	32.0	444	1	AJBSQU	glutamate-ammonia
41	805.5	32.0	491	2	E69368	glutamine syntheta
42	793	31.5	444	1	AJBSQS	glutamate-ammonia
43	780.5	31.0	454	2	A64468	glutamate-ammonia
44	765	30.4	439	2	B72313	glutamine syntheta
45	763	30.3	446	2	T46736	glutamate-ammonia

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:12:54 ; Search time 182 Seconds
(without alignments)
1342.098 Million cell updates/sec

Title: US-10-790-224A-20
Perfect score: 2517
Sequence: 1 VAFETPEEIVKFIKDENVF.....EISPVRLRPTPQEFELYFDC 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2513	99.8	477	2 Q79VE3	Q79ve3 corynebacte
2	2457	97.6	477	2 Q9Z474	Q9z474 corynebacte
3	2378	94.5	477	2 Q8FNP0	Q8fnp0 corynebacte
4	2036.5	80.9	478	2 Q6NG84	Q6ng84 corynebacte
5	1888.5	75.0	481	2 Q8FNM8	Q8fnm8 corynebacte
6	1838.5	73.0	478	2 Q939T2	Q939t2 mycobacteri
7	1789.5	71.1	478	1 GLN1_MYCTU	Q10377 mycobacteri
8	1778.5	70.7	478	2 Q9CCD8	Q9ccd8 mycobacteri
9	1777.5	70.6	478	2 Q73YJ4	Q73yj4 mycobacteri
10	1689	67.1	466	2 O85177	O85177 amycolatops
11	1654.5	65.7	469	1 GLNA_STRCO	P15106 streptomyce
12	1642.5	65.3	469	2 Q82AQ1	Q82aq1 streptomyce
13	1637.5	65.1	469	1 GLN1_STRRP	P77958 streptomyce
14	1618	64.3	478	2 Q8G5D8	Q8g5d8 bifidobacte
15	1598	63.5	474	2 Q6AFH0	Q6afh0 leifsonia x

complete seq

Jakoby

16	1592.5	63.3	469	1	GLN1_STRVR	Q05542	streptomyce
17	1555.5	61.8	473	2	Q6A9Y9	Q6a9y9	propionibac
18	1522	60.5	474	1	GLN1_FRAAL	P46033	frankia aln
19	1421	56.5	472	2	Q7NLR9	Q7nlr9	gloeobacter
20	1398.5	55.6	473	1	GLNA_SYNY3	P77961	synechocyst
21	1397	55.5	470	2	Q74C40	Q74c40	geobacter s
22	1394	55.4	470	1	GLNA_FREDI	P33035	fremyella d
23	1380.5	54.8	473	1	GLNA_SYNP2	P28605	synechococc
24	1376	54.7	471	2	Q8DIJ7	Q8dij7	synechococc
25	1363.5	54.2	473	1	GLNA_ANASP	P00964	anabaena sp
26	1357.5	53.9	476	2	Q89KR8	Q89kr8	bradyrhizob
27	1345.5	53.5	473	2	O50210	O50210	synechococc
28	1337	53.1	470	2	Q6MR33	Q6mr33	bdellovibri
29	1326.5	52.7	474	2	Q9RHZ1	Q9rhz1	anabaena az
30	1321.5	52.5	473	2	Q7V1F3	Q7v1f3	prochloroco
31	1313.5	52.2	491	2	Q8XRG8	Q8xrg8	ralstonia s
32	1311.5	52.1	473	2	Q7VBQ4	Q7vbq4	prochloroco
33	1310.5	52.1	473	2	Q7U7B2	Q7u7b2	synechococc
34	1310	52.0	474	2	Q83HM2	Q83hm2	tropheryma
35	1310	52.0	482	2	Q83GK6	Q83gk6	tropheryma
36	1301.5	51.7	473	2	Q7V7X8	Q7v7x8	prochloroco
37	1293.5	51.4	473	2	O31044	O31044	synechococc
38	1274.5	50.6	469	2	Q87TE8	Q87te8	vibrio para
39	1266	50.3	469	1	GLNA_AQUAE	O66514	aquifex aeo
40	1253.5	49.8	469	1	GLNA_VIBCH	Q9knj2	vibrio chol
41	1253.5	49.8	469	2	Q7MQ11	Q7mq11	vibrio vuln
42	1253.5	49.8	469	2	Q8DDR8	Q8ddr8	vibrio vuln
43	1252	49.7	468	1	GLNA_VIBAL	P19904	vibrio algi
44	1251.5	49.7	469	2	Q6LLR5	Q6llr5	photobacter
45	1242.5	49.4	469	2	Q8E976	Q8e976	shewanella